

SEQUENCE LISTING

<110> Reed, Guy L.

<120> Composition and Method for Enhancing Fibrinolysis

<130> 0609.4320003

<140>

<141> 2001-10-12

<150> 08/934,000

<151> 1997-09-19

<150> 60/026,356

<151> 1996-09-20

<160> 81

<170> PatentIn version 3.1

<210> 1

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> Alpha-2 Antiplasmin Antibody

<220>

<221> MISC_FEATURE

<222> (1)..(1)

<223> May be any Amino Acid

<400> 1

Xaa Ile Gln Met Thr Gln Ser Pro Ala Ser Leu Ser Ala Ser Val
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<210> 2

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Asp Ile Gln Met Thr
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<223> May be any Amino Acid

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Xaa Ile Gln Met Thr Gln Ser Pro Ala Ser Leu Ser Ala Ser Val
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<210> 4

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<222> (1)..(381)

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<222> (1)..(60)

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-20 -15 -10 -5

ggt gcc aga tgt gac atc cag atg act cag tct cca gcc tcc cta tct 96
Gly Ala Arg Cys Asp Ile Gln Met Thr Gln Ser Pro Ala Ser Leu Ser
1 5 10

gca tct gtg gga gaa act gtc acc atc aca tgt cga gca agt ggg aat 144
Ala Ser Val Gly Glu Thr Val Thr Ile Thr Cys Arg Ala Ser Gly Asn
15 20 25

att cac aat tat tta gca tgg tat cag cag aaa cag gga aaa tct cct 192
Ile His Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Gln Gly Lys Ser Pro
30 35 40

cag ctc ctg gtc tat aat gca aaa acc tta gca gat ggt gtg cca tca 240

Gln	Leu	Leu	Val	Tyr	Asn	Ala	Lys	Thr	Leu	Ala	Asp	Gly	Val	Pro	Ser	
45					50				55						60	
agg	ttc	agt	ggc	agt	gga	tca	gga	aca	caa	ttt	tct	ctc	agg	atc	aac	288
Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Gln	Phe	Ser	Leu	Arg	Ile	Asn	
					65				70					75		
agc	ctg	cag	cct	gaa	gat	ttt	ggg	agt	cat	tac	tgt	caa	cat	ttt	tgg	336
Ser	Leu	Gln	Pro	Glu	Asp	Phe	Gly	Ser	His	Tyr	Cys	Gln	His	Phe	Trp	
					80				85				90			
acc	act	ccg	tgg	acg	ttc	ggt	gga	ggc	acc	aag	ctg	gaa	atc	aaa	381	
Thr	Thr	Pro	Trp	Thr	Phe	Gly	Gly	Gly	Thr	Lys	Leu	Glu	Ile	Lys		
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<222> (9)..(9)

<223> May be either Gly or Ala

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Gly	Ala	Arg	Cys	Asp	Ile	Gln	Met	Thr	Gln	Ser	Pro	Ala	Ser	Leu	Ser
					1			5					10		

Ala	Ser	Val	Gly	Glu	Thr	Val	Thr	Ile	Thr	Cys	Arg	Ala	Ser	Gly	Asn
						15		20					25		

Ile	His	Asn	Tyr	Leu	Ala	Trp	Tyr	Gln	Gln	Lys	Gln	Gly	Lys	Ser	Pro
						30		35				40			

Gln	Leu	Leu	Val	Tyr	Asn	Ala	Lys	Thr	Leu	Ala	Asp	Gly	Val	Pro	Ser
45					50				55					60	

Arg Phe Ser Gly Ser Gly Thr Gln Phe Ser Leu Arg Ile Asn
65 70 75

Ser Leu Gln Pro Glu Asp Phe Gly Ser His Tyr Cys Gln His Phe Trp
80 85 90

Thr Thr Pro Trp Thr Phe Gly Gly Thr Lys Leu Glu Ile Lys
95 100 105

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<222> (1)..(381)

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<222> (1)..(60)

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-20 -15 -10 -5

48

ggt gcc aga tgt gac atc cag atg act cag tct cca gcc tcc cta tct
Gly Ala Arg Cys Asp Ile Gln Met Thr Gln Ser Pro Ala Ser Leu Ser
1 5 10

96

gca tct gtg gga gaa act gtc acc gtc aca tgt cga gca agt ggg aat
Ala Ser Val Gly Glu Thr Val Thr Val Cys Arg Ala Ser Gly Asn

144

15	20	25	
att cac aat tat tta gca tgg tat cag cag aaa cag gga aaa tct cct Ile His Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Gln Gly Lys Ser Pro			192
30	35	40	

cag ctc ctg gtc tat aat gca aga acc tta gca gat ggt gtg cca tca Gln Leu Leu Val Tyr Asn Ala Arg Thr Leu Ala Asp Gly Val Pro Ser			240
45	50	55	60

agg ttc agt ggc agt gga tca gga aca caa tat tct ctc aag atc aac Arg Phe Ser Gly Ser Gly Ser Gly Thr Gln Tyr Ser Leu Lys Ile Asn			288
65	70	75	

agc ctg cag cct gaa gat ttt ggg agt tat tac tgt caa cat ttt tgg Ser Leu Gln Pro Glu Asp Phe Gly Ser Tyr Tyr Cys Gln His Phe Trp			336
80	85	90	

agt aat ccg tgg acg ttc ggt gga ggc acc aag ctg gaa atc aaa Ser Asn Pro Trp Thr Phe Gly Gly Thr Lys Leu Glu Ile Lys			381
95	100	105	

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Met Ser Val Leu Thr Gln Val Leu Gly Leu Leu Leu Leu Trp Leu Thr			
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Gly Ala Arg Cys Asp Ile Gln Met Thr Gln Ser Pro Ala Ser Leu Ser			
1	5	10	

Ala Ser Val Gly Glu Thr Val Thr Val Thr Cys Arg Ala Ser Gly Asn			
15	20	25	

Ile His Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Gln Gly Lys Ser Pro			
30	35	40	

Gln Leu Leu Val Tyr Asn Ala Arg Thr Leu Ala Asp Gly Val Pro Ser			
45	50	55	60

Arg Phe Ser Gly Ser Gly Thr Gln Tyr Ser Leu Lys Ile Asn
65 70 75

Ser Leu Gln Pro Glu Asp Phe Gly Ser Tyr Tyr Cys Gln His Phe Trp
80 85 90

Ser Asn Pro Trp Thr Phe Gly Gly Thr Lys Leu Glu Ile Lys
95 100 105

<210> 8

<211> 381

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<220>

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<222> (1)..(381)

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Met Ser Val Leu Thr Gln Val Leu Ala Leu Leu Leu Leu Trp Leu Thr
-20 -15 -10 -5

48

ggt gcc aga tgt gac atc cag atg act cag tct cca gcc tcc cta tct
Gly Ala Arg Cys Asp Ile Gln Met Thr Gln Ser Pro Ala Ser Leu Ser
1 5 10

96

gca tct gtg gga gaa act gtc acc atc aca tgt cga gca agt ggg aat
Ala Ser Val Gly Glu Thr Val Thr Ile Thr Cys Arg Ala Ser Gly Asn
15 20 25

144

att cac aat tat tta gca tgg tat cag cag aaa cag gga aaa tct cct		192	
Ile His Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Gln Gly Lys Ser Pro			
30	35	40	
caa ctc ctg gtc tat aat gca aaa acc tta gca gat ggt gtg cca tca		240	
Gln Leu Leu Val Tyr Asn Ala Lys Thr Leu Ala Asp Gly Val Pro Ser			
45	50	55	60
agg ttc agt ggc agt gga tca gga aca caa ttt tct ctc aag atc aac		288	
Arg Phe Ser Gly Ser Gly Thr Gln Phe Ser Leu Lys Ile Asn			
65	70	75	
agc ctg cag cct gaa gat ttt ggg agt cat tac tgt caa cat ttt tgg		336	
Ser Leu Gln Pro Glu Asp Phe Gly Ser His Tyr Cys Gln His Phe Trp			
80	85	90	
acc act ccg tgg acg ttc ggt gga ggc acc aag ctg gaa atc aaa		381	
Thr Thr Pro Trp Thr Phe Gly Gly Thr Lys Leu Glu Ile Lys			
95	100	105	

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Met Ser Val Leu Thr Gln Val Leu Ala Leu Leu Leu Trp Leu Thr		
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Gly Ala Arg Cys Asp Ile Gln Met Thr Gln Ser Pro Ala Ser Leu Ser		
1	5	10

Ala Ser Val Gly Glu Thr Val Thr Ile Thr Cys Arg Ala Ser Gly Asn		
15	20	25

Ile His Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Gln Gly Lys Ser Pro		
30	35	40

Gln Leu Leu Val Tyr Asn Ala Lys Thr Leu Ala Asp Gly Val Pro Ser			
45	50	55	60

Arg Phe Ser Gly Ser Gly Thr Gln Phe Ser Leu Lys Ile Asn

65

70

75

Ser Leu Gln Pro Glu Asp Phe Gly Ser His Tyr Cys Gln His Phe Trp
80 85 90

Thr Thr Pro Trp Thr Phe Gly Gly Thr Lys Leu Glu Ile Lys
95 100 105

<210> 10

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-15 -10 -5

ctc caa gca cag atc cag ttg gtg cag tct gga cct gag ctg aag aag 96
Leu Gln Ala Gln Ile Gln Leu Val Gln Ser Gly Pro Glu Leu Lys Lys
1 5 10

cct gga gaa aca gtc aag atc tcc tgc aag gcc tct ggg tat acc ttc 144
Pro Gly Glu Thr Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe
15 20 25

aca aac tat gga atg aac tgg gtg aag cag gct cca gga aag ggt tta	192
Thr Asn Tyr Gly Met Asn Trp Val Lys Gln Ala Pro Gly Lys Gly Leu	
30 35 40 45	
aag tgg atg ggc tgg ata aac acc aag agt gga gag cca aca tat gct	240
Lys Trp Met Gly Trp Ile Asn Thr Lys Ser Gly Glu Pro Thr Tyr Ala	
50 55 60	
gaa gag ttc aag gga cgg ttt gtc ttc tct ttg gaa acc tct gcc agc	288
Glu Glu Phe Lys Gly Arg Phe Val Phe Ser Leu Glu Thr Ser Ala Ser	
65 70 75	
act gcc cat ttg cag atc aag aat ttc aga aat gag gac acg gct aca	336
Thr Ala His Leu Gln Ile Lys Asn Phe Arg Asn Glu Asp Thr Ala Thr	
80 85 90	
tat ttc tgt gca aga tgg gta cct ggg acc tat gct atg gac tac tgg	384
Tyr Phe Cys Ala Arg Trp Val Pro Gly Thr Tyr Ala Met Asp Tyr Trp	
95 100 105	
ggt caa gga acc tca gtc acc gtc tcc tca	414
Gly Gln Gly Thr Ser Val Thr Val Ser Ser	
110 115	

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<222> (2)..(2)
<223> May be either Asp or Ala
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<222> (6)..(6)
<223> May be either Asn or Thr

<220>
<223> Alpha-2 Antiplasmin Antibody
<400> 11

Met Xaa Trp Val Trp Xaa Leu Leu Phe Leu Met Ala Ala Ala Gln Ser

-15

-10

-5

Leu Gln Ala Gln Ile Gln Leu Val Gln Ser Gly Pro Glu Leu Lys Lys
1 5 10

Pro Gly Glu Thr Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe
15 20 25

Thr Asn Tyr Gly Met Asn Trp Val Lys Gln Ala Pro Gly Lys Gly Leu
30 35 40 45

Lys Trp Met Gly Trp Ile Asn Thr Lys Ser Gly Glu Pro Thr Tyr Ala
50 55 60

Glu Glu Phe Lys Gly Arg Phe Val Phe Ser Leu Glu Thr Ser Ala Ser
65 70 75

Thr Ala His Leu Gln Ile Lys Asn Phe Arg Asn Glu Asp Thr Ala Thr
80 85 90

Tyr Phe Cys Ala Arg Trp Val Pro Gly Thr Tyr Ala Met Asp Tyr Trp
95 100 105

Gly Gln Gly Thr Ser Val Thr Val Ser Ser
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<222> (1)..(57)

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<400> 12

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 -15 -10 -5

atc caa gca cag atc cag ttg gtg cag tct gga cct gag ctg aag aag 96
 Ile Gln Ala Gln Ile Gln Leu Val Gln Ser Gly Pro Glu Leu Lys Lys
 1 5 10

cct gga gag aca gtc aag atc tcc tgc aag gct tct ggg tat acc ttc
 Pro Gly Glu Thr Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe
 15 20 25

aca aag tat gga atg aac tgg gtg aag cag gct cca gga aag ggt tta
 Thr Lys Tyr Gly Met Asn Trp Val Lys Gln Ala Pro Gly Lys Gly Leu
 30 35 40 45

aag tgg atg ggc tgg ata aac acc aac agt gga gag cca aca tat gct 240
Lys Trp Met Gly Trp Ile Asn Thr Asn Ser Gly Glu Pro Thr Tyr Ala
50 55 60

gaa gag ttc aag gga cg^g ttt gcc ttc tct ttg gaa acc tct gcc agc 288
 Glu Glu Phe Lys Gly Arg Phe Ala Phe Ser Leu Glu Thr Ser Ala Ser
 65 70 75

act gcc tat ttg cag atc aac aac ctc aaa aat gag gac tcg gct aca 336
 Thr Ala Tyr Leu Gln Ile Asn Asn Leu Lys Asn Glu Asp Ser Ala Thr
 80 85 90

tat ttc tgt gca aga tgg gta cct ggg acc tat gct atg gac tac tgg 384
 Tyr Phe Cys Ala Arg Trp Val Pro Gly Thr Tyr Ala Met Asp Tyr Trp
 95 100 105

ggt caa gga acc tca gtc acc gtc tcc tca 414
Gly Gln Gly Thr Ser Val Thr Val Ser Ser
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<222> (2)..(2)

<223> May be either Asp or Ala

<220>

<221> MISC_FEATURE

<222> (6)..(6)

<223> May be either Asn or Thr

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<400> 13

Met Xaa Trp Val Trp Xaa Leu Leu Phe Leu Met Ala Ala Ala Gln Ser
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Ile Gln Ala Gln Ile Gln Leu Val Gln Ser Gly Pro Glu Leu Lys Lys
1 5 10

Pro Gly Glu Thr Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe
15 20 25

Thr Lys Tyr Gly Met Asn Trp Val Lys Gln Ala Pro Gly Lys Gly Leu
30 35 40 45

Lys Trp Met Gly Trp Ile Asn Thr Asn Ser Gly Glu Pro Thr Tyr Ala
50 55 60

Glu Glu Phe Lys Gly Arg Phe Ala Phe Ser Leu Glu Thr Ser Ala Ser
65 70 75

Thr Ala Tyr Leu Gln Ile Asn Asn Leu Lys Asn Glu Asp Ser Ala Thr
80 85 90

Tyr Phe Cys Ala Arg Trp Val Pro Gly Thr Tyr Ala Met Asp Tyr Trp
95 100 105

Gly Gln Gly Thr Ser Val Thr Val Ser Ser
110 115

<210> 14

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-15 -10 -5		
atc caa gca cag atc cag ttg gtg cag tct gga cct gag ctg aag aag		96
Ile Gln Ala Gln Ile Gln Leu Val Gln Ser Gly Pro Glu Leu Lys Lys		
1 5 10		
cct gga gaa aca gtc aag atc tcc tgc aag gct tct ggg tat acc ttc		144
Pro Gly Glu Thr Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe		
15 20 25		
aca aac tat gga atg aac tgg gtg aag cag gct cca gga aag ggt tta		192
Thr Asn Tyr Gly Met Asn Trp Val Lys Gln Ala Pro Gly Lys Gly Leu		
30 35 40 45		
aag tgg atg ggc tgg ata aac acc aag agt gga gag cca aca tat gct		240
Lys Trp Met Gly Trp Ile Asn Thr Lys Ser Gly Glu Pro Thr Tyr Ala		
50 55 60		
gaa gag ttc aag gga cgg ttt gcc ttc tct ttg gaa acc tct gcc agc		288
Glu Glu Phe Lys Gly Arg Phe Ala Phe Ser Leu Glu Thr Ser Ala Ser		
65 70 75		
act gcc aat ttg cag atc aag aac ctc aaa aat gag gac acg gct aca		336

Thr Ala Asn Leu Gln Ile Lys Asn Leu Lys Asn Glu Asp Thr Ala Thr
80 85 90

tat ttc tgt gca aga tgg gta cct ggg acc tat gcc atg gac tac tgg 384
Tyr Phe Cys Ala Arg Trp Val Pro Gly Thr Tyr Ala Met Asp Tyr Trp
95 100 105

ggt caa gga acc tca gtc acc gtc tcc tca 414
Gly Gln Gly Thr Ser Val Thr Val Ser Ser
110 115

<210> 15

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<222> (2)..(2)

<223> May be either Asp or Ala

<220>

<221> MISC_FEATURE

<222> (6)..(6)

<223> May be either Asn or Thr

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<223> Alpha-2 Antiplasmin Antibody

<400> 15

Met Xaa Trp Val Trp Xaa Leu Leu Phe Leu Met Ala Ala Ala Gln Ser
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Ile Gln Ala Gln Ile Gln Leu Val Gln Ser Gly Pro Glu Leu Lys Lys
1 5 10

Pro Gly Glu Thr Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe
15 20 25

Thr Asn Tyr Gly Met Asn Trp Val Lys Gln Ala Pro Gly Lys Gly Leu
30 35 40 45

Lys Trp Met Gly Trp Ile Asn Thr Lys Ser Gly Glu Pro Thr Tyr Ala
50 55 60

Glu Glu Phe Lys Gly Arg Phe Ala Phe Ser Leu Glu Thr Ser Ala Ser
65 70 75

Thr Ala Asn Leu Gln Ile Lys Asn Leu Lys Asn Glu Asp Thr Ala Thr
80 85 90

Tyr Phe Cys Ala Arg Trp Val Pro Gly Thr Tyr Ala Met Asp Tyr Trp
95 100 105

Gly Gln Gly Thr Ser Val Thr Val Ser Ser
110 115

<210> 16

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<212> DNA

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<223> Alpha-2 Antiplasmin Antibody

<220>

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<222> (31)..(411)

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<222> (31)..(90)

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<400> 16

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Met Ser Val Thr Gln Val Leu

54

-20 -15

gcg ttg ctg ctg ctg tgg ctt aca ggt gcc aga tgt gac atc cag atg 102
 Ala Leu Leu Leu Leu Trp Leu Thr Gly Ala Arg Cys Asp Ile Gln Met
 -10 -5 1

act cag tct cca tcc tcc cta tct gca tct gtg gga gac aga gtc acc 150
 Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr
 5 10 15 20

atc aca tgt cga gca agt ggg aat att cac aat tat tta gca tgg tat
 Ile Thr Cys Arg Ala Ser Gly Asn Ile His Asn Tyr Leu Ala Trp Tyr
 25 30 35

cag cag aaa cag gga aaa tct cct caa ctc ctg gtc tat aat gca aaa
 Gln Gln Lys Gln Gly Lys Ser Pro Gln Leu Leu Val Tyr Asn Ala Lys
 40 45 50

acc tta gca agt ggt gtg cca tca agg ttc agt ggc agt gga tca gga 294
 Thr Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly
 55 60 65

aca gat ttt act ctc acc atc agc agc ctg cag cct gaa gat ttt ggg 342
 Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Gly
 70 75 80

agt cat tac tgt caa cat ttt tgg acc act ccg tgg acg ttc ggt gga
 Ser His Tyr Cys Gln His Phe Trp Thr Thr Pro Trp Thr Phe Gly Gly
 85 90 95 100

ggc acc aag ctg gaa atc aaa 411
Gly Thr Lys Leu Glu Ile Lys
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<210> 17

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<223> Alpha-2 Antiplasmin Antibody

<400> 17

Met Ser Val Leu Thr Gln Val Leu Ala Leu Leu Leu Leu Trp Leu Thr
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Gly Ala Arg Cys Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser
1 5 10

Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gly Asn
15 20 25

Ile His Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Gln Gly Lys Ser Pro
30 35 40

Gln Leu Leu Val Tyr Asn Ala Lys Thr Leu Ala Ser Gly Val Pro Ser
45 50 55 60

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
65 70 75

Ser Leu Gln Pro Glu Asp Phe Gly Ser His Tyr Cys Gln His Phe Trp
80 85 90

Thr Thr Pro Trp Thr Phe Gly Gly Thr Lys Leu Glu Ile Lys
95 100 105

<210> 18

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<212> DNA

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<220>

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<222> (1)..(417)

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ggt gcc aga tgt cag atc cag ttg gtg cag tct gga tct gag ctg aag 96
Gly Ala Arg Cys Gln Ile Gln Leu Val Gln Ser Gly Ser Glu Leu Lys
1 5 10

aag cct gga gcc tca gtc aag atc tcc tgc aag gct tct ggg tat acc 144
Lys Pro Gly Ala Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr
15 20 25

ttc aca aac tat gga atg aac tgg gtg cga cag gct cca gga caa ggt 192
Phe Thr Asn Tyr Gly Met Asn Trp Val Arg Gln Ala Pro Gly Gln Gly
30 35 40

tta gag tgg atg ggc tgg ata aac acc aag agt gga gag cca aca tat 240
Leu Glu Trp Met Gly Trp Ile Asn Thr Lys Ser Gly Glu Pro Thr Tyr
45 50 55 60

gct gaa gag ttc aag gga cgg ttt gtc ttc tct ttg gac acc tct gtc 288
Ala Glu Glu Phe Lys Gly Arg Phe Val Phe Ser Leu Asp Thr Ser Val
65 70 75

acc act gcc tat ttg cag atc agc agc ctc aaa gct gag gac acg gct 336
Thr Thr Ala Tyr Leu Gln Ile Ser Ser Leu Lys Ala Glu Asp Thr Ala
80 85 90

gtg tat ttc tgt gca aga tgg gta cct ggg acc tat gcc atg gac tac 384
Val Tyr Phe Cys Ala Arg Trp Val Pro Gly Thr Tyr Ala Met Asp Tyr
95 100 105

tgg ggt caa gga acc acg gtc acc gtc tcc tca 417
Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
110 115

<210> 19

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<223> Alpha-2 Antiplasmin Antibody

<400> 19

Met Ser Val Leu Thr Gln Val Leu Ala Leu Leu Leu Leu Trp Leu Thr
-20 -15 -10 -5

Gly Ala Arg Cys Gln Ile Gln Leu Val Gin Ser Gly Ser Glu Leu Lys
1 5 10

Lys Pro Gly Ala Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr
15 20 25

Phe Thr Asn Tyr Gly Met Asn Trp Val Arg Gln Ala Pro Gly Gln Gly
30 35 40

Leu Glu Trp Met Gly Trp Ile Asn Thr Lys Ser Gly Glu Pro Thr Tyr
45 50 55 60

Ala Glu Glu Phe Lys Gly Arg Phe Val Phe Ser Leu Asp Thr Ser Val
65 70 75

Thr Thr Ala Tyr Leu Gln Ile Ser Ser Leu Lys Ala Glu Asp Thr Ala
80 85 90

Val Tyr Phe Cys Ala Arg Trp Val Pro Gly Thr Tyr Ala Met Asp Tyr
95 100 105

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
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<400> 21

Met Ser Val Leu Thr Gln Val Leu Ala Leu Leu Leu Trp Leu Thr
-20 -15 -10 -5

Gly Ala Arg Cys Gln Ile Gln Leu Val Gln Ser Gly Ala Glu Val Lys
1 5 10

Lys Pro Gly Ala Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr
15 20 25

Phe Thr Asn Tyr Gly Met Asn Trp Val Arg Gln Ala Pro Gly Gln Gly
30 35 40

Leu Glu Trp Met Gly Trp Ile Asn Thr Lys Ser Gly Glu Pro Thr Tyr
45 50 55 60

Ala Glu Glu Phe Lys Gly Arg Phe Thr Phe Thr Leu Asp Thr Ser Thr
65 70 75

Ser Thr Ala Tyr Leu Glu Ile Arg Ser Leu Arg Ser Asp Asp Thr Ala
80 85 90

Val Tyr Phe Cys Ala Arg Trp Val Pro Gly Thr Tyr Ala Met Asp Tyr
95 100 105

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
110 115

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33

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42

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actagtcgac atgagtgtgc tcactcaggt cctggsgttg

40

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tagggagacc caagcttgggt accaatttaa attgatatatct ccttaggtct cgagtctcta 60
gataaccgggt caatcgattt ggattttt 88

<210> 26

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gatccggcgcc aaaggcgcgc cgcaaggcac ccgggcttagc a

41

<210> 29
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32

<210> 30
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24

<210> 31
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<212> DNA

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gagatggagt ttgg 74

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<211> 72

<212> DNA

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attcgaagcc gg 72

<210> 33

<211> 24

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<400> 33

atcgatgcta gcaccaaggg cccca 24

<210> 34

<211> 24

<212> DNA

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<223> Alpha-2 Antiplasmin Antibody

<400> 34

ctcgaggggt caccacgctg ctga

24

<210> 35

<211> 21

<212> DNA

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<223> Alpha-2 Antiplasmin Antibody

<400> 35

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21

<210> 36

<211> 21

<212> DNA

<213> Artificial Sequence

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<223> Alpha-2 Antiplasmin Antibody

<400> 36

caccaggcct gtgcctgcct g

21

<210> 37

<211> 30

<212> DNA

<213> Artificial Sequence

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<400> 37

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30

<210> 38

<211> 80

<212> DNA

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<400> 38

cttgcggccg cttgctagca tggattgggt gtggaaacctg ctattcctga tggcagctgc

60

ccaaagtatac caagcacaga

80

<210> 39

<211> 80

<212> DNA

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ttggatactt tgggcagctg

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aactatggaa tgaactgggt

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<210> 41

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tcatatccata gtttgtgaag 80

<210> 42

<211> 80

<212> DNA

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<210> 43

<211> 80

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aaggcaaacc gtcccttgaa 80

<210> 44

<211> 80

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tgggacctat gccatggact 80

<210> 45

<211> 80

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<400> 45
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ggcataggta ccaggtaccc 80

<210> 46

<211> 29

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<400> 46
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<210> 47

<211> 30

<212> DNA

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<400> 47
atttaaattt atatctccctt aggtctcgag 30

<210> 48

<211> 79

<212> DNA

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<400> 48
atttaaattt atatctccctt aggtctcgag atgagtggtgc tcactcaggc cctggcgttt 60
ctgctgctgt ggcttacag 79

<210> 49

<211> 78

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<400> 49

agatgcagat agggaggctg gagactgagt catctggatg tcacatctgg cacctgtaag 60

ccacagcagc agcaacgc

78

<210> 50

<211> 78

<212> DNA

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<400> 50

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tggaaatatt cacaatta

78

<210> 51

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gaatattccc acttgctc

78

<210> 52

<211> 78

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<400> 52

aaatctccttc agtccttgtt ctataatgca aaaaccttag cagatggtgt gccatcaagg 60
ttcagtgccca gtggatca 78

<210> 53

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<400> 53

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ctgccactga accttgat 78

<210> 54

<211> 78

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cgttcggtgg aggcacca 78

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gcctccaccg aacgtccacg g

81

<210> 56

<211> 30

<212> DNA

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<400> 56

tcgattgacc ggtttatcttag agactcgaga 30

<210> 57

<211> 80

<212> DNA

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gcttacaggt gccagatgtc

80

<210> 58

<211> 80

<212> DNA

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ggcacctgtta agccacagca 80

<210> 59

<211> 80

<212> DNA

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<400> 59
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acaaaactatg gaatgaactg 80

<210> 60

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<400> 60
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ttccatagtt tgtgaaggta 80

<210> 61

<211> 80

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<400> 61

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agggacggtt tgtcttcct

80

<210> 62

<211> 80

<212> DNA

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acaaaccgtc ccttgaactc .

80

<210> 63

<211> 80

<212> DNA

<213> Artificial Sequence

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<400> 63

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acctgggacc tatgccatgg

80

<210> 64

<211> 80

<212> DNA

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<400> 64
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ataggtccca ggtacccatc 80

<210> 65

<211> 80

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agaaggcctgg agcctcagtc 80

<210> 66

<211> 80

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<400> 66
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agggacgggtt taccttcacc 80

<210> 67

<211> 80

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<400> 67

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gtaaaaccgtc ccttgaactc 80

<210> 68

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<400> 68

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acctgggacc tatgccatgg 80

<210> 69

<211> 78

<212> DNA

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<400> 69

agatgcagat agggaggatg gagactgagt catctggatg tcacatctgg cacctgttaag 60
ccacagcagc agcaacgc 78

<210> 70

<211> 78

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<400> 70

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tggaaatatt cacaatta 78

<210> 71

<211> 78

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<400> 71

aaatctcctc aactccttgtt ctataatgca aaaaccttag caagtggtgtt gccatcaagg 60
ttcagtgcca gtggatca 78

<210> 72

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<400> 72

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ctgccactga accttgat 78

<210> 73
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<400> 73

Tyr Pro Arg Ser Ile Tyr Ile Arg Arg Arg His Pro Ser Pro Ser Leu
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Thr Thr

<210> 74
<211> 15
<212> PRT
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<400> 74

Gly Gly Ser Gly Ser Gly Gly Ser Gly Ser Gly Gly Ser Gly Ser
1 5 10 15

<210> 75
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Glu Thr Val Thr Xaa Thr Cys Arg Ala Ser Gly Asn Ile His Asn Tyr
20 25 30

Leu Ala Trp Tyr Gln Gln Lys Gln Gly Lys Ser Pro Gln Leu Leu Val
35 40 45

Tyr Asn Ala Xaa Thr Leu Ala Asp Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Gln Xaa Ser Leu Xaa Ile Asn Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Gly Ser Xaa Tyr Cys Gln His Phe Trp Xaa Xaa Pro Trp
85 90 95

Thr Phe Gly Gly Thr Lys Leu Glu Ile Lys
100 105

<210> 76

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<223> May be any Amino Acid

<400> 76

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1 5 10 15

Glu Thr Val Thr Ile Thr Cys Arg Ala Ser Gly Asn Ile His Asn Tyr
20 25 30

Leu Ala Trp Tyr Gln Gln Lys Gln Gly Lys Ser Pro Gln Leu Leu Val
35 40 45

Tyr Asn Ala Lys Thr Leu Ala Asp Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Gln Phe Ser Leu Xaa Ile Asn Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Gly Ser His Tyr Cys Gln His Phe Trp Thr Thr Pro Trp
85 90 95

Thr Phe Gly Gly Thr Lys Leu Glu Ile Lys
100 105

<210> 77

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<400> 77

Asp Ile Gln Met Thr Gln Ser Pro Xaa Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Xaa Xaa Val Thr Xaa Thr Cys Arg Ala Ser Gly Asn Ile His Asn Tyr
20 25 30

Leu Ala Trp Tyr Gln Gln Lys Gln Gly Lys Ser Pro Gln Leu Leu Val
35 40 45

Tyr Asn Ala Xaa Thr Leu Ala Xaa Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Xaa Xaa Xaa Leu Xaa Ile Xaa Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Gly Ser Xaa Tyr Cys Gln His Phe Trp Xaa Xaa Pro Trp
85 90 95

Thr Phe Gly Gly Thr Lys Leu Glu Ile Lys
100 105

<210> 78

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1 5 10 15

Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asn Tyr
20 25 30

Gly Met Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Trp Ile Asn Thr Lys Ser Gly Glu Pro Thr Tyr Ala Glu Glu Phe
50 55 60

Lys Gly Arg Phe Xaa Phe Xaa Leu Asp Thr Ser Xaa Ser Thr Ala Tyr
65 70 75 80

Leu Xaa Ile Xaa Ser Leu Xaa Xaa Xaa Asp Thr Ala Val Tyr Phe Cys
85 90 95

Ala Arg Trp Val Pro Gly Thr Tyr Ala Met Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Thr Val Thr Val Ser Ser
115

<210> 79

<211> 119

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Thr Val Lys Ile Ser Cys Xaa Ala Ser Gly Tyr Thr Phe Thr Xaa Tyr
20 25 30

Gly Met Asn Trp Val Lys Gln Ala Pro Gly Lys Gly Leu Lys Trp Met
35 40 45

Gly Trp Ile Asn Thr Xaa Ser Gly Glu Pro Thr Tyr Ala Glu Glu Phe
50 55 60

Lys Gly Arg Phe Xaa Phe Ser Leu Glu Thr Ser Ala Ser Thr Ala Xaa
65 70 75 80

Leu Gln Ile Xaa Asn Xaa Asn Glu Asp Xaa Ala Thr Tyr Phe Cys
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35 40 45

Gly Trp Ile Asn Thr Lys Ser Gly Glu Pro Thr Tyr Ala Glu Glu Phe
50 55 60

Lys Gly Arg Phe Xaa Phe Ser Leu Glu Thr Ser Ala Ser Thr Ala Xaa
65 70 75 80

Leu Gln Ile Lys Asn Xaa Xaa Asn Glu Asp Thr Ala Thr Tyr Phe Cys
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Gly Met Asn Trp Val Xaa Gln Ala Pro Gly Xaa Gly Leu Xaa Trp Met
35 40 45

Gly Trp Ile Asn Thr Xaa Ser Gly Glu Pro Thr Tyr Ala Glu Glu Phe
50 55 60

Lys Gly Arg Phe Xaa Phe Xaa Leu Xaa Thr Ser Xaa Ser Thr Ala Xaa
65 70 75 80

Leu Xaa Ile Xaa Xaa Xaa Xaa Xaa Asp Xaa Ala Xaa Tyr Phe Cys
85 90 95

Ala Arg Trp Val Pro Gly Thr Tyr Ala Met Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Xaa Val Thr Val Ser Ser
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